

1/31

	130	140	150	160	
1093	GGGGAAACCCAGCACGAGT	GATGTCGTG	CTACCCGCAT	CT	M.tuberculosis
422	GGGGAAACCCAGCACGAGT	GATGTCGTG	TTACCCG	TATCT	M.avium
422	GGGGAAACCCAGCACGAGT	GATGTCGTG	TTACCCG	TATCT	M.paratuberc.
507	GGGGAAACCCAGCACGAGT	GATGTCGTG	TTACCC	AACGCT	M.phlei
432	GGGGAAACCCAGCACGAGT	GATGTCGTG	TTACCCG	TATCT	M.leprae
207	GGGGAAACCCAGCACGAGT	GATGTCGTG	TTACCCG	TATCT	M.gastri
150	GGGGAAACCCAGCACGAGT	GATGTCGTG	TTACCCGCATCT		M.kansasii
2588	GGGGAAACCCAGCACGAGT	GATGTCGTG	TTACCCAGGCGCT		M.smegmatis

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	210	220	230	240	
1172	CATCTCAGTACCCGTAGGA	AGAGAAAACAATTGTGATTCC			M.tuberculosis
501	CATCTCAGTACCCGTAGGA	AGAGAAAACAATTGTGATTCC			M.avium
501	CATCTCAGTACCCGTAGGA	AGAGAAAACAATTGTGATTCC			M.paratuberc.
586	CATCTCAGTACCCGTAGGA	AGAGAAAACAATTGTGATTCC			M.phlei
511	CATCTCAGTACCCGTAGGA	AGAGAAAACAATTGTGATTCC			M.leprae
286	CATCTCAGTACCCGTAGGA	AGAGAAAACAATTGTGATTCC			M.gastri
229	CATCTCAGTACCCGTAGGA	AGAGAAAACAATTGTGATTCC			M.kansasii
2667	CATCTCAGTACCCGTAGGA	AGAGAAAACAATTGTGATTCC			M.smegmatis

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	330	340	350	360	
1289	TGTGGGAG-GATATGTCTCAGCGCTACCCGGCTGAGA-GG				M.tuberculosis
617	TGTGGGATTGATATGTCTCAGCTCTACCTGGCTGAGG-GG				M.avium
617	TGTGGGATTGATATGTCTCAGCTCTACCTGGCTGAGG-GG				M.paratuberc.
703	TGTGGGSCCTGTGTGTC-CATCGTCCGCCGATGGCAG				M.phlei
629	TGTGGGATTGATATGTCTCACTCTACCTGGCTGAGG-GG				M.leprae
404	TGTGGGATCGATACTCTCAGCTCTACCCGGCTGAGG-GG				M.gastri
347	TGTGGGATCGATACTCTCAGCTCTACCCGGCTGAGG-GG				M.kansasii
2785	TGTGGGACCTATCTTTC-CCTCTACCTGGCTG-GAGGG				M.smegmatis

Figure 1A

2/31

	370	380	390	400	
1327	CAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M. tuberculosis
656	TAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M. avium
656	TAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M. paratuberc.
742	TAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M. phlei
668	TAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M. leprae
443	CAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M. gastri
386	CAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M. kansasii
2823	CAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M. smegmatis

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	450	460	470	480	
1406	CGGCACCTGCCTTATATCAATTC	CGAGTAGCAGCGGGCC			M. tuberculosis
735	CGGCACCTGCCTTATATCAATTC	CGAGTAGCAGCGGGCC			M. avium
735	CGGCACCTGCCTTATATCAATTC	CGAGTAGCAGCGGGCC			M. paratuberc.
820	TGCTGCCGCTGTACAGG--T	CGAGTAGCAGCGGGCC			M. phlei
747	TGGCACCTGCCTTGTATCAATTC	CGAGTAGCAGCGGGCC			M. leprae
522	CGGCACCTGCCTTGTATCAATTC	CGAGTAGCAGCGGGCC			M. gastri
465	CGGCACCTGCCTTGTATCAATTC	CGAGTAGCAGCGGGCC			M. kansasii
2902	CGACGTCTGCTTGTATGGTG	TCCCGAGTAGCAGCGGGCC			M. smegmatis

	490	500	510	520	
1446	CGTGGAATCTGCTGTGAATCTG	CCGGGACCACCGGTAAG			M. tuberculosis
775	CGTGGAATCTGCTGTGAATCTG	CCGGGACCACCGGTAAG			M. avium
775	CGTGGAATCTGCTGTGAATCTG	CCGGGACCACCGGTAAG			M. paratuberc.
857	CGTGGAATCTGCTGTGAATCTG	CCGGGACCACCGGTAAG			M. phlei
787	CGTGGAATCTGCTGTGAATCTG	CCGGGACCACCGGTAAG			M. leprae
562	CGTGGAATCTGCTGTGAATCTG	CCGGGACCACCGGTAAG			M. gastri
505	CGTGGAATCTGCTGTGAATCTG	CCGGGACCACCGGTAAG			M. kansasii
2942	CGTGGAATCTGCTGTGAATCTG	CCGGGACCACCGGTAAG			M. smegmatis

Figure 1B

3/31

	610	620	630	640	
1566	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCC	TCCT			M. tuberculosis
894	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. avium
894	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. paratuberc.
976	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCC	CTCT			M. phlei
907	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. leprae
682	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCC	CTCT			M. gastri
625	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCCTTT				M. kansasii
3062	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCCTCT	CT			M. smegmatis
	650	660	670	680	
1606	TTTCCTCTCCCGAGGAGGGT	GGTGATGGCGTGCCTTTTGA			M. tuberculosis
934	C-----	GTGGGGTGATGGCGTGCCTTTTGA			M. avium
934	C-----	GTGGGGTGATGGCGTGCCTTTTGA			M. paratuberc.
1016	CTT-----	GTAGTGGGGTGATGGCGTGCCTTTTGA			M. phlei
947	T-----	GTGGGGTGATGGCGTGCCTTTTGA			M. leprae
722	T-----	GTGGGGTGATGGCGTGCCTTTTGA			M. gastri
665	C-----	GTGGGGTGATGGCGTGCCTTTTGA			M. kansasii
3102	ACGTGT-----	GTGGGGTGATGGCGTGCCTTTTGA			M. smegmatis
	690	700	710	720	
1646	AGAATGAGCCTGCGAGTCAGGGACAT	TGTCGCA	AGGTTAAC		M. tuberculosis
4	AGAATGAGCCTGCGAGTCAGGGACAT	TGTCGCA	AGGTTAAC		M. bovis
959	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. avium
23	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. intracellular
959	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. paratuberc.
1046	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. phlei
972	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. leprae
747	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. gastri
690	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. kansasii
3132	AGAATGAGCCTGCGAGTCAGGGACAT	GTTCGCA	AGGTTAAC		M. smegmatis

Figure 1C

### Figure 1D

5/31

	1130	1140	1150	1160	
2082	ACAGCCCAGATCGCCGGCTAAGGCC	CAAGCGTGTGCTA	M.tuberculosis		
1385	ACAGCCCAGATCGCCGGCTAAGGCC	CAAGCGTGTGCTA	M.avium		
1385	ACAGCCCAGATCGCCGGCTAAGGCC	CAAGCGTGTGCTA	M.paratuberc.		
1479	ACAGCCCAGATCGCCGGCTAAGGCC	CAAGCGTGTGCTA	M.phlei		
1401	ACAGCCCAGATCGCCGGCTAAGGCC	CAAGCGTGTGCTA	M.leprae		
1175	ACAGCCCAGATCGCCGGCTAAGGCC	CAAGCGTGTGCTA	M.gastri		
1118	ACAGCCCAGATCGCCGGCTAAGGCC	CAAGCGTGTGCTA	M.kansasii		
3566	ACAGCCCAGATCGCCGGCTAAGGCC	CAAGCGTGTGCTA	M.smegmatis		

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	1290	1300	1310	1320	
2241	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CCACCTTGT-	M.tuberculosis		
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.avium		
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.paratuberc.		
1638	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.phlei		
1560	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.leprae		
1334	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.gastri		
1277	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.kansasii		
3726	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA	M.smegmatis		

	1330	1340	1350	1360	
2280	-GGTGGGTG	TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.tuberculosis		
1583	CGGTGGAT	TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.avium		
1583	CGGTGGAT	TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.paratuberc.		
1676	TGGCTGGT	TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.phlei		
1600	GGGTGGAT	TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.leprae		
1367	AGGT----	TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.gastri		
1310	AGGT----	TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.kansasii		
3764	TT-----	TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.smegmatis		

Figure 1E

6/31

	1370	1380	1390	1400	
2319	CCAC	GGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.tuberculosis
1623	CT	CCGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.avium
1623	CT	CCGGGTGATCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.paratuberc.
1716	CCGCCG	AGTGATCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.phlei
1640	CC	CCGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M.leprae
1402	CCGCCGGT	GACCGGTGGTGGAGGATGGGGGAGTGAGAAT			M.gastri
1345	CTGCCGGT	GACCGGTGGTGGAGGATGGGGGAGTGAGAAT			M.kansasii
3796	CCGCCG	AGTATCGAGTGGTGGAGGGTGGGGGAGTGAGAAT			M.smegmatis

	1410	1420	1430	1440	
2359	GCAGGCATGAGTAGCGA	CAAGGCAAGTGAGAACCTTGCCC			M.tuberculosis
1662	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.avium
1662	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.paratuberc.
1756	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTCCC			M.phlei
1680	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.leprae
1442	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.gastri
1385	GCAGGCATGAGTAGCGA	TAAGGCAAGTGAGAACCTTGCCC			M.kansasii
3836	GCAGGCATGAGTAGCGA	TTAGGCAAGTGAGAACCTTCCC			M.smegmatis

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	1570	1580	1590	1600	
2519	CGCCCGTGAC	GAATCA-GCGGTACTAACCACCCAAAACCG			M.tuberculosis
1821	CGTCCCTGATGAATCA	-GCGGTACTAACCACCCAAAACCG			M.avium
1821	CGTCCCTGATGAATCA	-GCGGTACTAACCACCCAAAACCG			M.paratuberc.
1915	CGTCCCTGATGAATCA	TCATTCTGCTAACCACCCAAAACCG			M.phlei
1840	CGCCCGTGATGAATCA	-GCGGTACTAACCACCCAAAACCG			M.leprae
1602	CGCCCGTGATGAATCA	-GCGGTACTAACCACCCAAAACCG			M.gastri
1545	CGCCCGTGATGAATCA	-GCGGTACTAACCACCCAAAACCG			M.kansasii
3996	CGTCCATGATGAATCA	-GCGGTACTAACCACCCAAAACCG			M.smegmatis

Figure 1F

### Figure 1G

### Figure 1H



## Figure 11

10/31

	2970	2980	2990	3000	
3904	GTTGTCCCG	CCAGGGGCACCGCTGGATAGCCACGTTTCGGT			M.tuberculosis
3203	GTTGTCCCA	CCAGGGGCACCGCTGGATAGCCACGTTTCGGG			M.avium
3203	GTTGTCCCA	CCAGGGGCACCGCTGGATAGCCACGTTTCGGG			M.paratuberc.
3296	GTTGTCCCA	CCAGGGGCACCGCTGGATAGCCACGTTTCGGG			M.phlei
3227	GTTGTCT	CCAGGGGCACCGCTGGATAGCCACGTTTCGGG			M.leprae
1910					M.gastri
2931	GTTGTCCCA	CCAGGGGCACCGCTGGATAGCCACGTTTCGGG			M.kansasii
5382	GTTGTCCCA	CCAGGGGCACCGCTGGATAGCCACGTTTCGGG			M.smegmatis
	3010	3020	3030	3040	
3944	CAGSATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.tuberculosis
3243	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.avium
3243	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.paratuberc.
3336	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.phlei
3267	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.leprae
1910					M.gastri
2971	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.kansasii
5422	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.smegmatis
- - - -					
	3090	3100	3110	3120	
4023	CCCGC-AGAACACGGGTTCAATAGGT	CAGACCTGGAAGCT			M.tuberculosis
609	CCCGC-AGAACACGGGTTCAATAGGT	CAGACCTGGAAGCT			M.bovis
3322	CCCGC-AGAACACGGGTTGATAGG	CAGACCTGGAAGCT			M.avium
677	CCCGC-AGAACACGGGTTGATAGG	CAGACCTGGAAGCT			M.intracellulare
3322	CCCGC-AGAACACGGGTTGATAGG	CAGACCTGGAAGCT			M.paratuberc.
3415	CCCGC-AGAACACGGGTTGATAGG	CAGACCTGGAAGCT			M.phlei
3309					M.leprae
1910					M.gastri
3050	CCCGC-AGAACACGGGTTGATAGG	CAGACCTGGAAGCT			M.kansasii
5501	CCCGC-AGAACACGGGTTGATAGG	CAGACCTGGAAGCT			M.smegmatis

Figure 1J

11/31

	50	60	70	80	
2	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAG	GTCTC			M.tuberculosis
141	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.bovis
39	GCGGCGTACTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.avium
1	-----TTAACACATGCAAGTGAACGGAAAG	ACCC			M.intracellulare
39	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.paratuberc.
2	GCGGCGTGCTTAACAATGCAAGTCGAACGGAAAGGTCTC				M.scrofulaceum
40	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.leprae
2	CGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.kansasii
2	GCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.gastri
40	GCGGCGTGCTTAACACATGCAAGTCGAACGGTAAGGTCTC				M.gordonae
1	-----GTGCTTAACACATGCAAGTCGAACGGAAAGGTCTC				M.marinum
	90	100	110	120	
42	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.tuberculosis
181	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.bovis
79	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.avium
32	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.intracellulare
79	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.paratuberc.
42	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.scrofulaceum
80	TAAAAAATCTTTTATAGATACTCGAGTGGCGAACGGGT				M.leprae
41	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.kansasii
42	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.gastri
80	-----GCGGTACACGAGTGGCGAACGGGT				M.gordonae
36	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.marinum
	130	140	150	160	
70	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.tuberculosis
209	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.bovis
107	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.avium
59	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.intracellulare
107	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.paratuberc.
70	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.scrofulaceum
120	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.leprae
69	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.kansasii
70	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.gastri
104	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.gordonae
64	GAGTAACACGTGGGTGATCTGCCCTGCACTTC-GGGATAA				M.marinum

Figure 2A

12/31

	170	180	190	200	
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGAC	CACGGGA			M.tuberculosis
248	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M.bovis
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTTCAAGA				M.avium
98	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTTTAGG				M.intracellulare
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTTCAAGA				M.paratuberc.
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACCTTGG				M.scrofulaceum
160	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTTCAAGG				M.leprae
108	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACCTTGG				M.kansasii
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACCTTGG				M.gastri
143	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACCTGGA				M.gordonae
103	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M.marinum
	210	220	230	240	
149	TGCATGTCTTGTGGTGGAAAGCGCTTTAG	CGGTGTGGGAT			M.tuberculosis
288	TGCATGTCTTGTGGTGGAAAGCGCTTTAGCGGTGTGGGAT				M.bovis
186	CGCATGTCTTGTGGTGGAAAGCTTTTACGGTGTGGGAT				M.avium
138	CGCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.intracellulare
186	CGCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.paratuberc.
149	CGCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.scrofulaceum
200	CGCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.leprae
148	CGCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.kansasii
149	CGCATGTCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.gastri
183	CACATGTCCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.gordonae
143	TTCATGTCCTTGTGGTGGAAAGCTTTTGC	CGGTGTGGGAT			M.marinum
	250	260	270	280	
189	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.tuberculosis
328	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.bovis
224	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.avium
176	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.intracellulare
224	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.paratuberc.
187	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.scrofulaceum
239	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.leprae
186	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.kansasii
187	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.gastri
221	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.gordonae
181	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.marinum

Figure 2B

13/31

	450	460	470	480	
389	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.tuberculosis
528	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.bovis
424	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.avium
376	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.intracellulare
424	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.paratuberc.
387	AAACCTCTTTACCATCGACGAAGGTCTCA				M.scrofulaceum
439	AAACCTCTTTACCATCGACGAAGGTCTGGG				M.leprae
386	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.kansasii
387	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.gastri
420	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.gordonae
381	AAACCTCTTTACCATCGACGAAGGTCCGGGTT				M.marinum

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	1130	1140	1150	1160	
1069	TCTCATGTTGCCAGCACGTAATGGT				M.tuberculosis
1208	TCTCATGTTGCCAGCACGTAATGGT				M.bovis
1104	TCTCATGTTGCCAGCACGTAATGGT				M.avium
1056	TCTCATGTTGCCAGCACGTAATGGT				M.intracellulare
1098	TCTCATGTTGCCAGCACGTAATGGT				M.paratuberc.
1064	TCTCATGTTGCCAGCACGTAATGGT				M.scrofulaceum
1119	TCTCATGTTGCCAGCACGTAATGGT				M.leprae
1066	TCTCATGTTGCCAGCACGTAATGGT				M.kansasii
1067	TCTCATGTTGCCAGCACGTAATGGT				M.gastri
1100	TCTCATGTTGCCAGCACGTAATGGT				M.gordonae
1061	TCTCATGTTGCCAGCACGTAATGGT				M.marinum

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	1250	1260	1270	1280	
1189	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.tuberculosis
1328	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.bovis
1224	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.avium
1176	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.intracellulare
1218	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.paratuberc.
1184	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.scrofulaceum
1239	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.leprae
1186	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.kansasii
1187	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.gastri
1220	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.gordonae
1181	CAATGGCCGGTACAAAGGGCTGCGATGCCG				M.marinum

Figure 2C

### Figure 2D

15/31

		50	60	70	80	
128	TTCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC					M.tuberculosis
39	TGCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC					M.bovis
41	TCCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC					M.phlei
3559	TACCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC					M.leprae
5743	TCCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC					M.smegmatis

		90	100	110	120	
168	TGCCCCTCCGGG---TGGAAAAGTAGGACACCGCCGAAC					M.tuberculosis
79	TGCCCCTCCGGG---TGGAAAAGTAGGACACCGCCGAAC					M.bovis
81	TGCCCCTCCGGG---TGGAAAAGTAGGACACCGCCGAAC					M.phlei
3599	TGCCCCTCCGGG---TGGAAAAGTAGGACACCGCCGAAC					M.leprae
5782	TGCCCCTCCGGG---TGGAAAAGTAGGACACCGCCGAAC					M.smegmatis

Figure 3

16/31

	90	100	110	120	
382	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.avium
382	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.paratuberc.
1053	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.tuberculosis
467	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.phlei
392	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.leprae
167	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.gastri
110	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.kansasii
2548	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATT	TCCGAAT		M.smegmatis

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	170	180	190	200	
462	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.avium
462	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.paratuberc.
1133	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.tuberculosis
547	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.phlei
472	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.leprae
247	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.gastri
190	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.kansasii
2628	GAATATATAGGGTGCG-GGAGG	TAAACGCGGGGAAGTGAAA			M.smegmatis

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	250	260	270	280	
541	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.avium
541	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.paratuberc.
1212	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.tuberculosis
626	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.phlei
551	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.leprae
326	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.gastri
269	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.kansasii
2706	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.smegmatis

Figure 4A



17/31

	290	300	310	320	
578	CATG	CATGGACA	ACCGGGTAGGGGTTGTGTGTGCGGGGT		M. avium
578	CATG	CATGGACA	ACCGGGTAGGGGTTGTGTGTGCGGGGT		M. paratuberc.
1250	CAAG	CATGGGT	AACCGGGTAGGGGTTGTGTGTGCGGGGT		M. tuberculosis
664	CGTG	CATGTGAT	ACCGGGTAGGGGTTGTGTGTGCGGGGT		M. phlei
590	CACA	CATGTCTAAC	TAGGTAGGGGTTGTGTGTGCGGGGT		M. leprae
365	CAAG	CATGGGT	AACCGGGTAGGGGTTGTGTGTGCGGGGT		M. gastri
308	CAAG	CATGGGT	AACCGGGTAGGGGTTGTGTGTGCGGGGT		M. kansasii
2745	TATGA	CATGTGAT	ACCGGGTAGGGGTTGTGTGTGCGGGGT		M. smegmatis

	330	340	350	360	
617	TGTGGG	ATTGATATG	TCTCAG	TCTACCTGGCTGAGG	-GG M. avium
617	TGTGGG	ATTGATATG	TCTCAG	TCTACCTGGCTGAGG	-GG M. paratuberc.
1289	TGTGGG	AGG	GATATGTCTCAG	CTACCTGGCTGAGG	-GG M. tuberculosis
703	TGTGGG	CCCTGT	TGTCTCAG	CTACCTGGCTGAGG	-GG M. phlei
629	TGTGGG	ATTGAT	ATGCTCAG	CTACCTGGCTGAGG	-GG M. leprae
404	TGTGGG	ATTGAT	ATGCTCAG	CTACCTGGCTGAGG	-GG M. gastri
347	TGTGGG	ATTGAT	ATGCTCAG	CTACCTGGCTGAGG	-GG M. kansasii
2785	TGTGGG	ATTGAT	ATGCTCAG	CTACCTGGCTGAGG	-GG M. smegmatis

	370	380	390	400	
656	TAGTCAGAAAGT	GTCTGGTTAGCGGAAGTGGCCTGGGAT			M. avium
656	TAGTCAGAAAGT	GTCTGGTTAGCGGAAGTGGCCTGGGAT			M. paratuberc.
1327	CAGTCAGAAAGT	GTCTGGTTAGCGGAAGTGGCCTGGGAT			M. tuberculosis
742	TAGTCAGAAAGT	GTCTGGTTAGCGGAAGTGGCCTGGGAT			M. phlei
668	TAGTCAGAAAGT	GTCTGGTTAGCGGAAGTGGCCTGGGAT			M. leprae
443	CAGTCAGAAAGT	GTCTGGTTAGCGGAAGTGGCCTGGGAT			M. gastri
386	CAGTCAGAAAGT	GTCTGGTTAGCGGAAGTGGCCTGGGAT			M. kansasii
2823	CAGTCAGAAAGT	GTCTGGTTAGCGGAAGTGGCCTGGGAT			M. smegmatis

Figure 4B

18/31

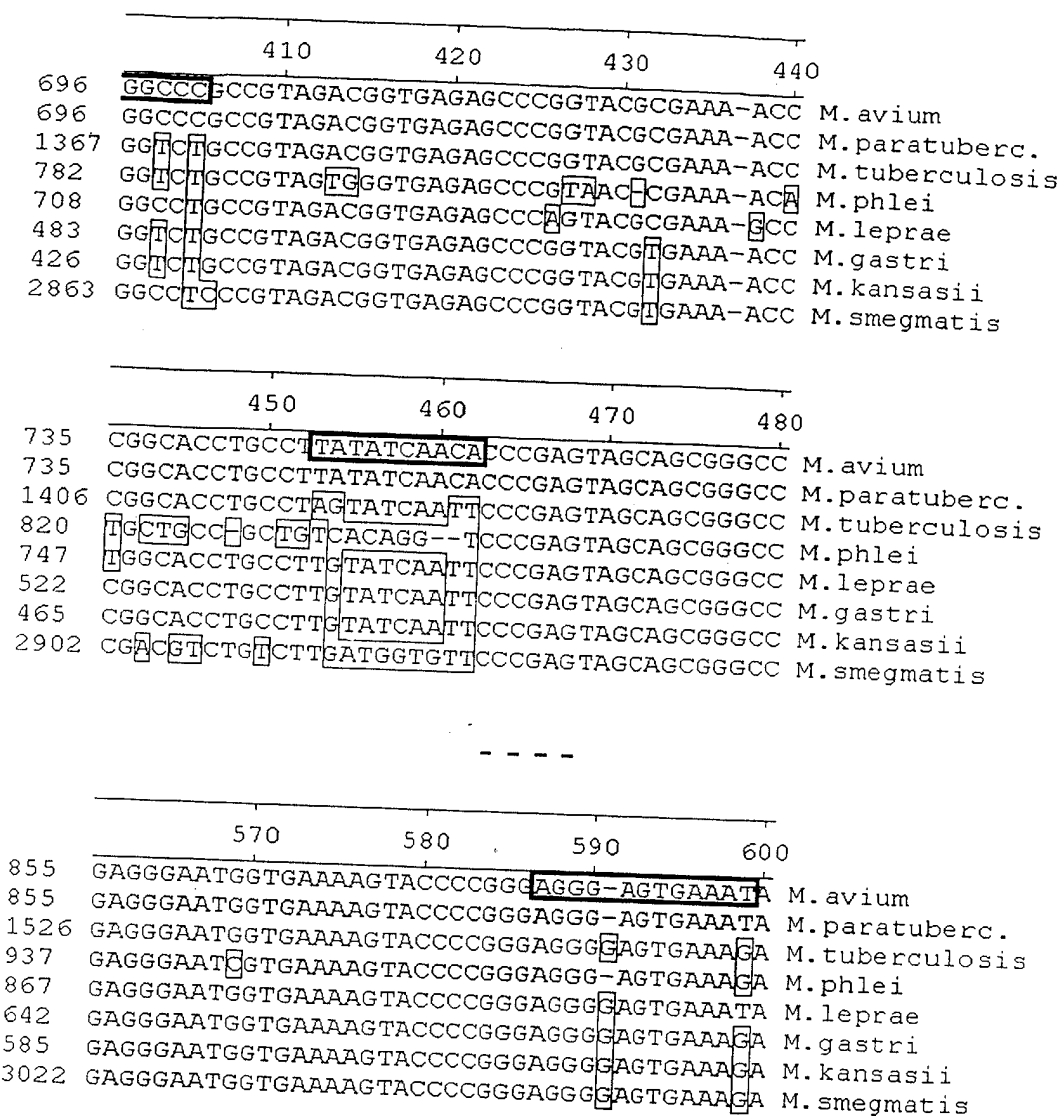


Figure 4C

19/31

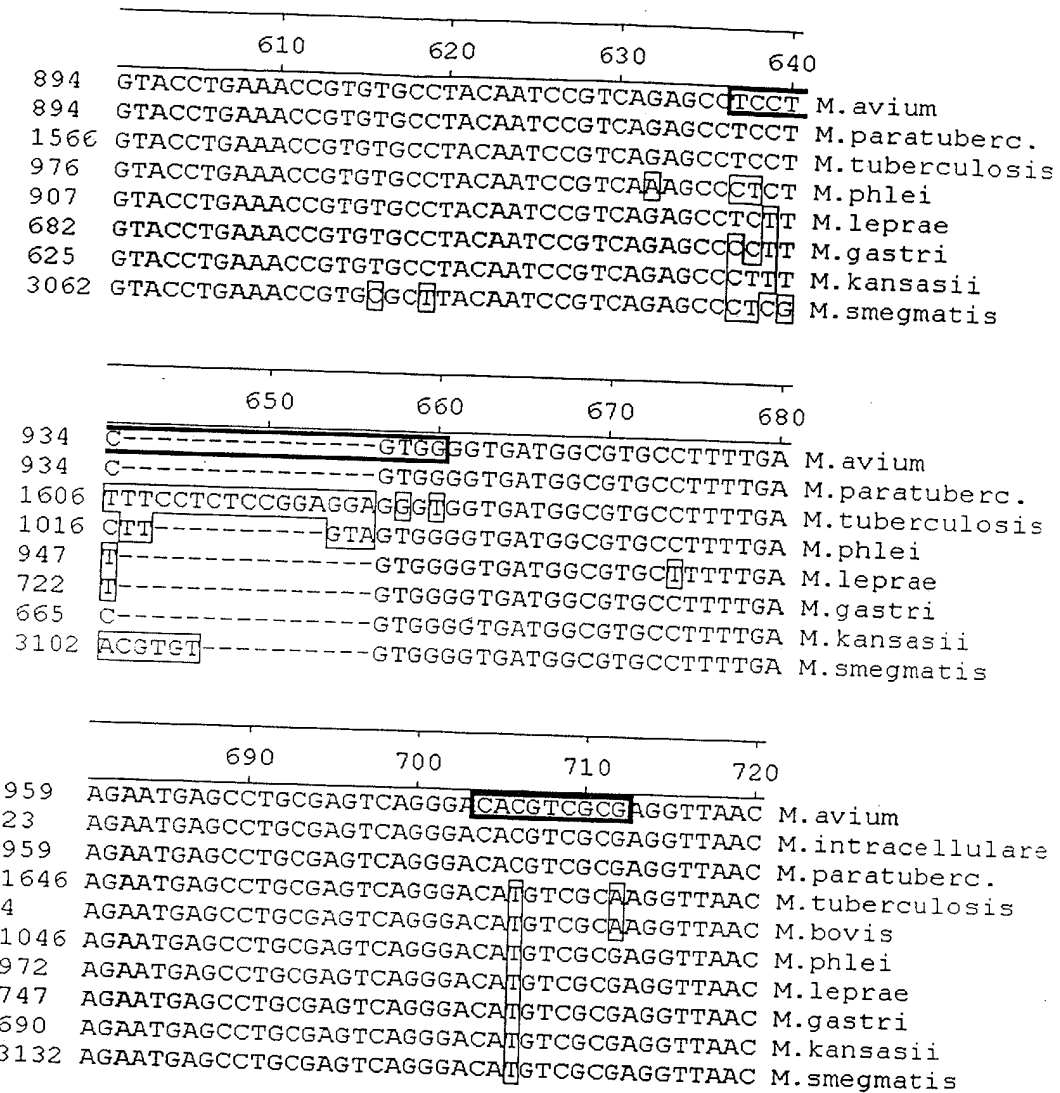


Figure 4D

APPROVED FOR RELEASE  
 CLASS  
 DATE 11-11-81

20/31

	770	780	790	800	
1039	CGCATCCCCTTTGGG	-----	GTG	TAGTGGCGTGT	M. avium
103	CGCATCCCCTTTGGG	-----	GTG	TAGTGGCGTGT	M. intracellulare
1039	CGCATCCCCTTTGGG	-----	GTG	TAGTGGCGTGT	M. paratuberc.
1726	CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT				M. tuberculosis
84	CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT				M. bovis
1126	CGTATCCAACCTGTT	-----	GGGGTTG	GTGTAGTGGGTGTGT	M. phlei
1052	CGTATCACGTTGTGAGCGT	-----		GTGTAGTGGCGTGT	M. leprae
827	CGTATCACGCGTAAGCGT	-----		GTGTAGTGGCGTGT	M. gastri
770	CGTATCGCGCGGAGCGT	-----		GTGTAGTGGCGTGT	M. kansasii
3212	CGTATCCACACAAGAGTGTGTG	-----		GTGTAGTGGGTGTGT	M. smegmatis

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	1050	1060	1070	1080	
1307	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGC	GTGGCA		M. avium
1307	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCGTGGCA			M. paratuberc.
2005	CAGCCAAACTCCGAATGCCG	TGGTG-TA	AAGCGTGGCA		M. tuberculosis
1401	CAGCCAAACTCCGAATGCCG	TAAG-T	AAAAGGTGGCA		M. phlei
1323	CAGCCAAACTCCGAATGCCG	TGGT-T	AAAAGCGTGGCA		M. leprae
1098	CAGCCAAACTCCGAATGCCG	TGGTG-TATA	GCGTGGCA		M. gastri
1041	CAGCCAAACTCCGAATGCCG	TGGTG-TATA	GCGTGGCA		M. kansasii
3486	CAGCCAAACTCCGAATGCCG	TAAGCCAAGAGTGGGA			M. smegmatis

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	1170	1180	1190	1200	
1425	AGTGGAAAAGGATGTGT	TAGTCGCAGA	-GACAACCAGGAGG		M. avium
1425	AGTGGAAAAGGATGTGT	TAGTCGCAGA	-GACAACCAGGAGG		M. paratuberc.
2122	AGTGGAAAAGGATGTGT	CAGTCGCAGA	-GACAACCAGGAGG		M. tuberculosis
1519	AGTGGAAAAGGATGTGT	CAGTCGCAGA	-GACAACCAGGAGG		M. phlei
1441	AGTGGAAAAGGATGTGT	CAGTCGCAGA	-GACAACCAGGAGG		M. leprae
1215	AGTGGAAAAGGATGTGT	CAGTCGCAGA	-GACAACCAGGAGG		M. gastri
1158	AGTGGAAAAGGATGTGT	CAGTCGCAGA	-GACAACCAGGAGG		M. kansasii
3606	AGTGGAAAAGGATGTGT	CAGTCGCAGA	-GACAACCAGGAGG		M. smegmatis

Figure 4E

21/31

	1250	1260	1270	1280	
1504	CTCACTGGTCAAGTGATT	ATGCGCC	TATAATGTAGCGGGG		M. avium
1504	CTCACTGGTCAAGTGATT	TATGCGCCGATAATGTAGCGGGG			M. paratuberc.
2201	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGGG			M. tuberculosis
1598	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGGG			M. phlei
1520	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGGG			M. leprae
1294	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGGG			M. gastri
1237	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGGG			M. kansasii
3686	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGGG			M. smegmatis

	1290	1300	1310	1320	
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M. avium
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M. paratuberc.
2241	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M. tuberculosis
1638	CTCAAGCACACCGCCGAAGCCGCGGC	ATCAGCTTTT			M. phlei
1560	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M. leprae
1334	CTCAAGCACACCGCCGAAGCCGCGGC	CA-----ACCGC--A			M. gastri
1277	CTCAAGCACACCGCCGAAGCCGCGGC	CA-----ACCGC--A			M. kansasii
3726	CTCAAGCACACCGCCGAAGCCGCGGC	CA-----ACCGC--A			M. smegmatis

	1330	1340	1350	1360	
1583	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTCAGCGAAG		M. avium
1583	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTCAGCGAAG		M. paratuberc.
2280	GGTGGTGTGGGTAGGGGAGCGT	CCCC	CATTCAGCGAAG		M. tuberculosis
1676	TGGCTGTGTGGGTAGGGGAGCGT	CCCC	CATTCAGCGAAG		M. phlei
1600	GGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTCAGCGAAG		M. leprae
1367	AGGT-----TGGGTAGGGGAGCGT	CCCC	CATTCAGCGAAG		M. gastri
1310	AGGT-----TGGGTAGGGGAGCGT	CCCC	CATTCAGCGAAG		M. kansasii
3764	TT-----TGGGTAGGGGAGCGT	CCCC	CATTCAGCGAAG		M. smegmatis

Figure 4F

22/31

	1370	1380	1390	1400	
1623	CT-C	CGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M. avium
1623	CT-CCGGGTGA	CGGTGGTGGAGGGTGGGGGAGTGAGAAT			M. paratuberc.
2319	CCACCGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT				M. tuberculosis
1716	CCGCCG	GTGA	CGGTGGTGGAGGGTGGGGGAGTGAGAAT		M. phlei
1640	CCTCCGGGT	AACCGGTGGTGGAGGGTGGGG	AGTGAGAAT		M. leprae
1402	CCGCCGGGTGACCGGTGGTGGAGG	ATGGGGGAGTGAGAAT			M. gastri
1345	CTGCCGGGTGACCGGTGGTGGAGG	ATGGGGGAGTGAGAAT			M. kansasii
3796	CCGCCG	AGTAT	CGAGTGGTGGAGGGTGGGGAGTGAGAAT		M. smegmatis

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	1530	1540	1550	1560	
1781	CGATGGACAACGGGTTGATATTCCCGTACCCGTGT	ATGGG			M. avium
1781	CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG				M. paratuberc.
2479	CGATGGACAACGGGTTGATATTCCCGTACCCGTGT	GTGGG			M. tuberculosis
1875	CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATG	AG			M. phlei
1800	CGATGGACAACGGGTTGATATTCCCGTACCCGTGT	GTGGG			M. leprae
1562	CGATGGACAACGGGTTGATATTCCCGTACCCGTGT	GTGGG			M. gastri
1505	CGATGGACAACGGGTTGATATTCCCGTACCCGTGT	GTGGG			M. kansasii
3956	CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATG	AG			M. smegmatis

	1570	1580	1590	1600	
1821	CGTCCCTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M. avium
1821	CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG				M. paratuberc.
2519	CGCCCTGA	GAATCA-GCGGTACTAACCACCCAAAACCG			M. tuberculosis
1915	CGTCCCTGATGAATC	TCATTCT	CTAACCACCCAAAACCG		M. phlei
1840	CGCCCTGATGAATCA-GCGGTACT	ACCACCCAAAACCG			M. leprae
1602	CGCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG				M. gastri
1545	CGCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG				M. kansasii
3996	CGTCCATGATGAATCA-GCGGTACTAACCA	CCAAAACCG			M. smegmatis

Figure 4G

23/31

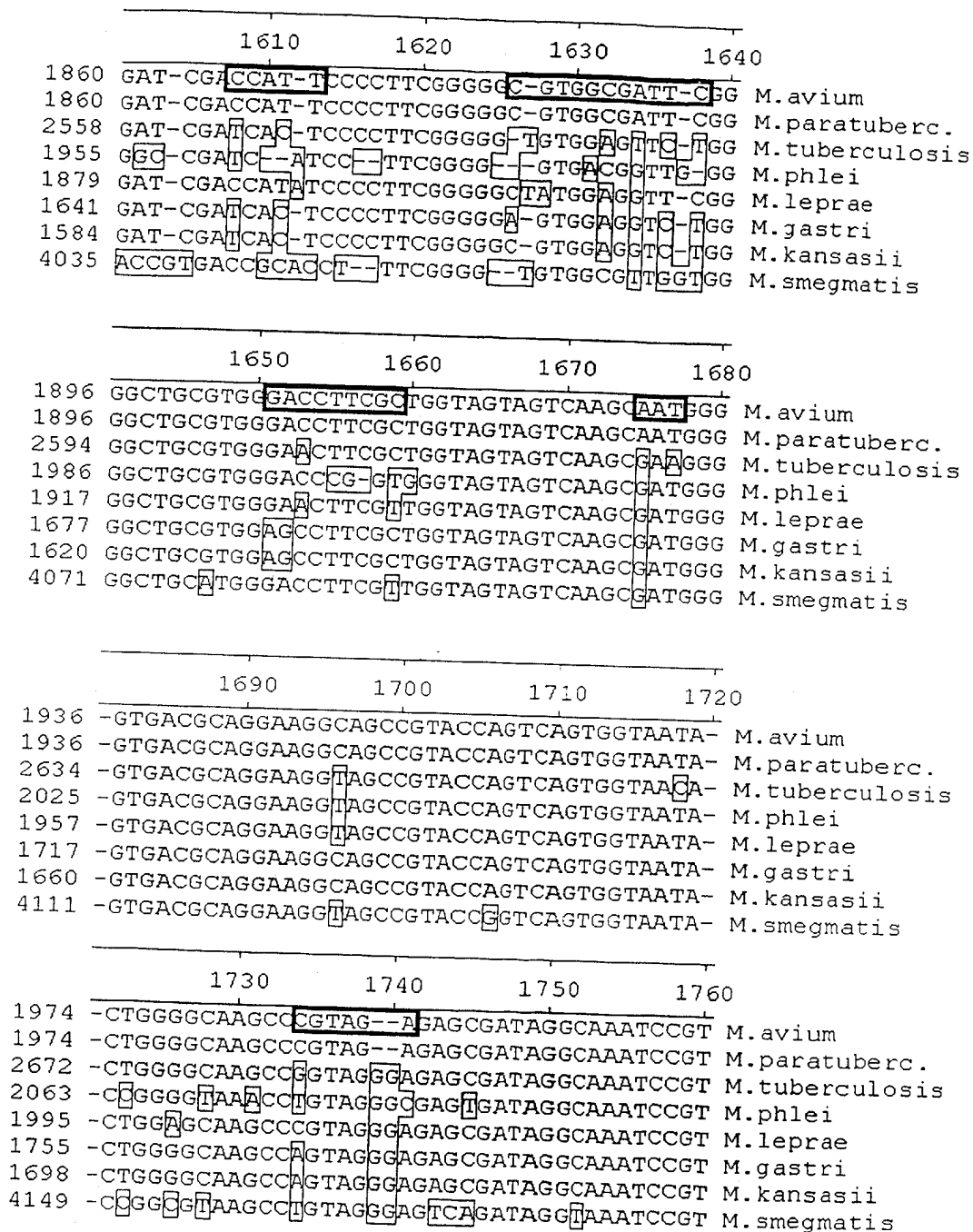


Figure 4H

24/31

	1810	1820	1830	1840	
2051	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. avium
2051	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. paratuberc.
2751	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. tuberculosis
2141	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. phlei
2074	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. leprae
1834	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. gastri
1777	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. kansasii
4228	CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. smegmatis
	1850	1860	1870	1880	
2089	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. avium
2089	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. paratuberc.
2789	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. tuberculosis
2179	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. phlei
2112	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. leprae
1872	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. gastri
1815	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. kansasii
4266	GCGAGCACATACACGCGCCCGTACCCCAAACCAACACAGGT				M. smegmatis
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	1970	1980	1990	2000	
2208	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. avium
2208	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. paratuberc.
2908	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. tuberculosis
2298	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. phlei
2231	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. leprae
1910					M. gastri
1934	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. kansasii
4385	AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC				M. smegmatis
	2010	2020	2030	2040	
2248	GGGATTCGGGTCGCAGAAACCAAGTGGTGGCGACT-GTTTA				M. avium
2248	GGGATTCGGGTCGCAGAAACCAAGTGGTGGCGACT-GTTTA				M. paratuberc.
2948	GGGATTCGGGTCGCAGAAACCAAGTGGTGGCGACT-GTTTA				M. tuberculosis
2338	GGGATTCGGGTCGCAGAAACCAAGTGGTGGCGACT-GTTTA				M. phlei
2271	GGGATTCGGGTCGCAGAAACCAAGTGGTGGCGACT-GTTTA				M. leprae
1910					M. gastri
1974	GGGATTCGGGTCGCAGAAACCAAGTGGTGGCGACT-GTTTA				M. kansasii
4425	GGGATTCGGGTCGCAGAAACCAAGTGGTGGCGACT-GTTTA				M. smegmatis

Figure 41



25/31

	2130	2140	2150	2160	
2367	CCGTTAACCC	GT	--AAGGGTGAAGCGGAGAATTTAAGCCC		M.avium
2367	CCGTTAACCCGT	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.paratuberc.
3067	CCGTTAACCCG	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.tuberculosis
2457	CCGTTAACCC	TTTCGG	GGGTGAAGCGGAGAATTTAAGCCC		M.phlei
2390	C	GT	TAAACCCGA	--AAGGGTGAAGCGGAGAATTTAAGCCC	M.leprae
1910					M.gastri
2094	CCGTTAACCCG	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.kansasii
4544	CCGTTAACCC	CCTTGG	GGGTGAAGCGGAGAATTTAAGCCC		M.smegmatis

	2250	2260	2270	2280	
2485	GTAACGACTTC	CCAA	CTGTCTCAACCATAGACTCGGCGAA		M.avium
2485	GTAACGACTTCCCA	ACTGTCTCAACCATAGACTCGGCGAA			M.paratuberc.
3185	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.tuberculosis
2577	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.phlei
2508	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.leprae
1910					M.gastri
2212	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.kansasii
4663	GTAACGACTTC	CAACTGTCTCAAC	ATAGACTCGGCGAA		M.smegmatis

	2370	2380	2390	2400	
2605	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.avium
2605	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACTTTGAA				M.paratuberc.
3305	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.tuberculosis
2697	G	TCG	ATACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA	M.phlei
2628	GTTTCGGT	CGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA		M.leprae
1910					M.gastri
2332	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.kansasii
4782	G	TCG	ATACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA	M.smegmatis

Figure 4J

REF ID: A66822  
 CLASS  
 RAFTS:

26/31

	2410	2420	2430	2440	
2645	GCACA	SACGCCAGTT	CTGT	GGAGTCGTTGTTGAAATACC	M.avium
393	ATACAGACGCCAGTTTGT	ATGGAGTCGTTGTTGAAATACC			M.intracellulare
2645	GCACAGACGCCAGTTTGT	TGGAGTCGTTGTTGAAATACC			M.paratuberc.
3345	ACCTCGACGCCAGTTGGGG	GGAGTCGTTGTTGAAATACC			M.tuberculosis
284	ACCTCGACGCCAGTTGGGG	GGAGTCGTTGTTGAAATACC			M.bovis
2737	GCTCGACGCCAGTTGGGG	TGGAGTCGTTGTTGAAATACC			M.phlei
2668	ACTTCGACGC	TAGTTGGGTGGAGTCGTTGTTGAAATACC			M.leprae
1910					M.gastri
2372	ACCTCAACGCCAGTTGGGG	TGGAGTCGTTGTTGAAATACC			M.kansasii
4822	GCTCAACGCCAGTGTGG	TGGAGTCGTTGTTGAAATACC			M.smegmatis

	2450	2460	2470	2480	
2685	ACTCTGATCGTATTGGACACCTAACGTCGAAC	CT-TATC			M.avium
433	ACTCTGATCGTATTGGACACCTAACGTCGAAC	CCCT-TATC			M.intracellulare
2685	ACTCTGATCGTATTGGACACCTAACGTCGAAC	CCCT-TATC			M.paratuberc.
3385	ACTCTGATCGTATTGGGCATCTAACCTCGAAC	CCCTGAATC			M.tuberculosis
324	ACTCTGATCGTATTGGGCATCTAACCTCGAAC	CCCTGAATC			M.bovis
2777	ACTCTGATCGTATTGGGCCTCTAACCTCGAAC	CTGGATC			M.phlei
2708	ACTCTGATCTGATTGACATCTAACCTCGAAC	CTATATC			M.leprae
1910					M.gastri
2412	ACTCTGATCGTATTGGACACCTAACGTCGAAC	CCCTGAATC			M.kansasii
4862	ACTCTGATCGTATTGGGCCTCTAACCTCGAAC	CTATATC			M.smegmatis

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	2690	2700	2710	2720	
2924	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAAC	GG			M.avium
2924	GGTGTCACTCAACGGATAAAAGGTACCCCGGGGATAAC	AG			M.paratuberc.
3625	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAAC	AG			M.tuberculosis
3017	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAAC	AG			M.phlei
2948	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAAC	AG			M.leprae
1910					M.gastri
2652	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAAC	AG			M.kansasii
5102	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAAC	AG			M.smegmatis

	2730	2740	2750	2760	
2964	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.avium
2964	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.paratuberc.
3665	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.tuberculosis
3057	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.phlei
2988	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.leprae
1910					M.gastri
2692	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.kansasii
5142	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M.smegmatis

Figure 4K

27/31

	2770	2780	2790	2800	
3004	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M. avium
3004	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M. paratuberc.
3705	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M. tuberculosis
3097	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M. phlei
3028	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M. leprae
1910					M. gastri
2732	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M. kansasii
5182	GCACCTCGATGT	CGGCTCGTCGC	ATCCTGGGGCT	GGAGCA	M. smegmatis
	2810	2820	2830	2840	
3044	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATTAA	AGCGGCAC	M. avium
3044	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATTAA	AGCGGCAC	M. paratuberc.
3745	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATTAA	AGCGGCAC	M. tuberculosis
3137	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATTAA	AGCGGCAC	M. phlei
3068	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATTAA	AGCGGCAC	M. leprae
1910					M. gastri
2772	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATTAA	AGCGGCAC	M. kansasii
5222	GGTCCCAAGG	TGGGCTGTT	CGCCC-ATTAA	AGCGGCAC	M. smegmatis
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	3050	3060	3070	3080	
3283	CAAGATCAGGTTT	-CTCACCC	TTT	TAGAGGGATAAGGCC	M. avium
638	CAAGATCAGGTTT	-CTCACCC	TTT	TAGAGGGATAAGGCC	M. intracellulare
3283	CAAGATCAGGTTT	-CTCACCC	TTT	TAGAGGGATAAGGCC	M. paratuberc.
3984	CAAGATCAGGTTT	-CTCACCC	TTT	TAGAGGGATAAGGCC	M. tuberculosis
570	CAAGATCAGGTTT	-CTCACCC	TTT	TAGAGGGATAAGGCC	M. bovis
3376	CAAGATCAGGTTT	-CTCACCC	TTT	TAGAGGGATAAGGCC	M. phlei
3307	CAA				M. leprae
1910					M. gastri
3011	CAAGATCAGGTTT	-CTCACCC	TTT	TAGAGGGATAAGGCC	M. kansasii
5462	CAAGATCAGGTTT	-CTCACCC	TTT	TAGAGGGATAAGGCC	M. smegmatis
	3090	3100	3110	3120	
3322	CCCGC-AGACCACGGG	ATTGATAGGC	CAGACCTGGAAGCT		M. avium
677	CCCGC-AGACCACGGG	ATTGATAGGC	CAGACCTGGAAGCT		M. intracellulare
3322	CCCGC-AGACCACGGG	ATTGATAGGC	CAGACCTGGAAGCT		M. paratuberc.
4023	CCCGC-AGACCACGGG	ATTGATAGGC	CAGACCTGGAAGCT		M. tuberculosis
609	CCCGC-AGACCACGGG	ATTGATAGGC	CAGACCTGGAAGCT		M. bovis
3415	CCCGC-AGACCACGGG	ATTGATAGGC	CAGACCTGGAAGCT		M. phlei
3309					M. leprae
1910					M. gastri
3050	CCCGC-AGACCACGGG	ATTGATAGGC	CAGACCTGGAAGCT		M. kansasii
5501	CCCGC-AGACCACGGG	ATTGATAGGC	CAGACCTGGAAGCT		M. smegmatis

Figure 4L

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	130	140	150	160	
107	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA	M.avium
59	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.intracellulare
107	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.paratuberc.
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.scrofulaceum
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.tuberculosis
209	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.bovis
120	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.leprae
69	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.kansasii
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.gastri
104	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.gordonae
64	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.marinum
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	450	460	470	480	
424	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTT	CTCGG		M.avium
376	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTTCTCGG			M.intracellulare
424	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTTCTAGG			M.paratuberc.
387	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTCTAGG			M.scrofulaceum
389	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTCTCGG			M.tuberculosis
528	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTCTCGG			M.bovis
439	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTCTCGG			M.leprae
386	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTCTCGG			M.kansasii
387	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTCTCGG			M.gastri
420	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTCTCGG			M.gordonae
381	AAACCTCTTTACCATCGACGAAGGTCCGGG	TTTCTCGG			M.marinum
	490	500	510	520	
429	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.tuberculosis
568	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.bovis
464	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.avium
416	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.intracellulare
464	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.paratuberc.
424	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.scrofulaceum
479	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.leprae
426	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.kansasii
427	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.gastri
460	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.gordonae
421	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG				M.marinum

Figure 5A

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	1130	1140	1150	1160	
1104	TCTCATGTTGCCAGC	GGGTAATGC	CGGGGACTCGTGAGAG		M.avium
1056	TCTCATGTTGCCAGC	GGGTAATGCCGGGGACTCGTGAGAG			M.intracellulare
1098	TCTCATGTTGCCAGC	GGGTAATGC	CGGGGACTCGTGAGAG		M.paratuberc.
1064	TCTCATGTTGCCAGC	GGGTAATGCCGGGGACTCGTGAGAG			M.scrofulaceum
1069	TCTCATGTTGCCAGC	AGTAATG	STGGGGACTCGTGAGAG		M.tuberculosis
1208	TCTCATGTTGCCAGC	AGTAATG	STGGGGACTCGTGAGAG		M.bovis
1119	TCTCATGTTGCCAGC	AGTAATG	STGGGGACTCGTGAGAG		M.leprae
1066	TCTCATGTTGCCAGC	GGGTAATGCCGGGGACTCGTGAGAG			M.kansasii
1067	TCTCATGTTGCCAGC	GGGTAATGCCGGGGACTCGTGAGAG			M.gastri
1100	TCTCATGTTGCCAGC	GGGTAATGCCGGGGACTCGTGAGAG			M.gordonae
1061	TCTCATGTTGCCAGC	AGTAATG	STGGGGACTCGTGAGAG		M.marinum

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	1290	1300	1310	1320	
1264	CGAATCCTTTTA	AAGCCGGACTCAGTTCGGAT	TGGGGTCT		M.avium
1216	CGAATCCTTTTA	AAGCCGGTCTCAGTTCGGATTGGGGTCT			M.intracellulare
1258	CGAATCCTTTTA	AAGCCGGACTCAGTTCGGATTGGGGTCT			M.paratuberc.
1224	CGAATCCTTTTA	AAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.scrofulaceum
1229	CGAATCCTTTA	AAAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.tuberculosis
1368	CGAATCCTTTA	AAAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.bovis
1279	CGAATCCTTTTA	AAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.leprae
1226	CGAATCCTTTTA	AAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.kansasii
1227	CGAATCCTTTTA	AAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.gastri
1260	CGAATCCTTTTA	AAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.gordonae
1221	CGAATCCTTT	AAAGCCGGTCTCAGTTCGGAT	TGGGGTCT		M.marinum

	1330	1340	1350	1360	
1304	GCAACTCGACCCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M.avium
1256	GCAACTCGACCCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M.intracellulare
1298	GCAACTCGACCCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M.paratuberc.
1264	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.scrofulaceum
1268	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.tuberculosis
1407	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.bovis
1319	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.leprae
1266	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.kansasii
1267	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.gastri
1300	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.gordonae
1260	GCAACTCGACCCC	GTGAAGTCGGAGTCGCTAGTAATCGCA			M.marinum

Figure 5B

FIG. 6  
SUBCLASS

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2550 2568 2589

2550 | TTACGGCGGCAGGACGAAAGACCCCGGACCTTACTA | 2589

2568 2569

Mavium 23S:

Figure 6

M. tuberculosis 16S:

441 | TGGAGAGAAAGCACC GGCCAACTACGTGCCAGCAGC GCGGTAAATACGTAG 491  
452 | 473 474 477 |

843 | GTACGGCCGCAAGCTAAAACTCAAAGGAATTGACGGGGGC 883  
865 866 | |

## Figure 7